

SEQUENCE LISTING

67094 U.S. PTO
08853684
05/09/97



(1) GENERAL INFORMATION

(i) APPLICANT: DEEN, KEITH C
YOUNG, PETER R

(ii) TITLE OF THE INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR, TR6

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: RATNER & PRESTIA
- (B) STREET: P.O. BOX 980
- (C) CITY: VALLEY FORGE
- (D) STATE: PA
- (E) COUNTRY: USA
- (F) ZIP: 19482

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: TO BE ASSIGNED
- (B) FILING DATE: 09-MAY-1997
- (C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/041,230
- (B) FILING DATE: 14-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: PRESTIA, PAUL F.
- (B) REGISTRATION NUMBER: 23,031
- (C) REFERENCE/DOCKET NUMBER: GH-50008

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-407-0700
- (B) TELEFAX: 610-407-0701
- (C) TELEX: 846169

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3,881 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTTGCGCCC ACAAAATACA CCGACGATGC CCGATCTACT TTAAGGGCTG AAACCCACGG	60
GCCTGAGAGA CTATAAGAGC GTTCCCTACC GCCATGGAAC AACGGGGACA GAACGCCCG	120
GCCGCTTCGG GGGCCCGGAA AAGGCACGGC CCAGGACCCA GGGAGGCGCG GGGAGCCAGG	180
CCTGGGCCCC GGGTCCCCAA GACCCCTGTG CTCGTTGTCG CCGCGGTCTT GCTGTTGGTC	240
TCAGCTGAGT CTGCTCTGAT CACCCAAACAA GACCTAGCTC CCCAGCAGAG AGCGGCCCA	300
CAACAAAAGA GGTCCAGCCC CTCAGAGGGA TTGTGTCCAC CTGGACACCA TATCTCAGAA	360
GACGGTAGAG ATTGCATCTC CTGCAAATAT GGACAGGACT ATAGCACTCA ATGGAATGAC	420
CTCCTTTCT GCTTGCCTG CACCAAGGTGT GATTCAAGGTG AAGTGGAGCT AAGTCCCTGC	480
ACCACGACCA GAAACACAGT GTGTCAGTGC GAAGAAGGCA CCTTCCGGGA AGAAGATTCT	540
CCTGAGATGT GCCGGAAGTG CCGCACAGGG TGTCCCAGAG GGATGGTCAA GGTCGGTGAT	600
TGTACACCCT GGAGTGACAT CGAATGTGTC CACAAAGAAT CAGGCATCAT CATAGGAGTC	660
ACAGTTGCAG CCGTAGTCTT GATTGTGGCT GTGTTGTTT GCAAGTCTT ACTGTGGAAG	720

AAAGTCCTTC	CITACCTGAA	AGGCATCTGC	TCAGGTGGTG	GTGGGGACCC	TGAGCGTGTG	780
GACAGAAGCT	CACAACGACC	TGGGGCTGAG	GACAATGTCC	TCAATGAGAT	CGTGAGTATC	840
TTGCAGCCCA	CCCAGGTCCC	TGAGCAGGAA	ATGGAAGTCC	AGGAGCCAGC	AGAGCCAACA	900
GGTGTCAACA	TGTTGTCCCC	CGGGGAGTCA	GAGCATTGTC	TGGAACCGGC	AGAAGCTGAA	960
AGGTCTCAGA	GGAGGAGGCT	GCTGGTTCCA	GCAAATGAAG	GTGATCCCAC	TGAGACTCTG	1020
AGACAGTGCT	TCGATGACTT	TGCAGACTTG	GTGCCCTTG	ACTCCTGGGA	GCCGCTCATG	1080
AGGAAGTTGG	GCCTCATGGA	CAATGAGATA	AAGGTGGCTA	AAGCTGAGGC	AGCGGGCCAC	1140
AGGGACACCT	TGTACACGAT	GCTGATAAAAG	TGGGTCAACA	AAACCGGGCG	AGATGCCTCT	1200
GTCCACACCC	TGCTGGATGC	CITGGAGACG	CTGGGAGAGA	GACTTGCCAA	GCAGAAGATT	1260
GAGGACCACT	TGTTGAGCTC	TGGAAAGTTC	ATGTATCTAG	AAGGTAATGC	AGACTCTGCC	1320
ATGTCCTAAG	TGTGATTCTC	TTCAGGAAGT	CAGACCTTCC	CTGGTTTACC	TTTTTTCTGG	1380
AAAAAGCCCA	ACTGGACTCC	AGTCAGTAGG	AAAGTGCCAC	AATTGTCACA	TGACCGGTAC	1440
TGGAAGAAC	TCTCCCATCC	AACATCACCC	AGTGGATGGA	ACATCCTGTA	ACTTTTCACT	1500
GCACATTGGCA	TTATTTTAT	AAAGCTGAATG	TGATAATAAG	GACACTATGG	AAATGTCCTGG	1560
ATCAATTCCGT	TTGTGCGTAC	TTTGAGATTT	GGTTTGGGAT	GTCATTGTTT	TCACAGCACT	1620
TTTTTATCCT	AATGTAAATG	CTTTATTTAT	TTATTTGGC	TACATTGTAA	GATCCATCTA	1680
CACAGTCGTT	GTCCGACTTC	ACTTGATACT	ATATGATATG	AACCTTTTT	GGGTGGGGGG	1740
TGCGGGGCAG	TTCACTCTGT	CTCCCAGGCT	GGAGTGCAAT	GGTGAATCT	TGGCTCACTA	1800
TAGCCTTGAC	CTCTCAGGCT	CAAGCGATT	TCCCACCTCA	GCCATCCAAA	TAGCTGGAC	1860
CACAGGTGTG	CACCAACCACG	CCCGGCTAAT	TTTTTGTAIT	TTGTCTAGAT	ATAGGGCTC	1920
TCTATGTTGC	TCAGGGTGGT	CTCGAATTCC	TGGACTCAAG	CAGTCIGCCC	ACCTCAGACT	1980
CCCAAAGCGG	TGGAATTAGA	GGCGTGAGCC	CCCATGCTTG	GCCTTACCTT	TCTACTTTA	2040
TAATTCTGTA	TGTTATTATT	TTATGAACAT	GAAGAAACTT	TAGTAAATGT	ACTTGTTAC	2100
ATAGTTATGT	GAATAGATTA	GATAAACATA	AAAGGAGGAG	ACATACAATG	GGGAAAGAAG	2160
AAGAAGTCCC	CTGTAAGATG	TCACTGTCTG	GGTTCCAGCC	CTCCCTCAGA	TGTACTTTGG	2220
CITCAATGAT	TGGCAACTTC	TACAGGGGCC	AGTCTTTGA	ACTGGACAAC	CITACAAGTA	2280
TATGAGTATT	ATTTATAGGT	AGTTGTTTAC	ATATGAGTCG	GGACCAAAGA	GAACCTGGATC	2340
CACGTGAAGT	CCTGTGTGTG	GCTGGTCCCT	ACCTGGCAG	TCTCATTGTC	ACCCATAGCC	2400
CCCATCTATG	GACAGGCTGG	GACAGAGGCA	GATGGGTTAG	ATCACACATA	ACAATAGGGT	2460
CTATGTCATA	TCCCAAGTGA	ACTTGAGCCC	TGTTTGGCT	CAGGAGATAG	AAGACAAAAT	2520
CTGTCTCCCC	ACGTCTGCCA	TGGCATCAAG	GGGGAAGAGT	AGATGGTGT	TGAGAATGGT	2580
GTGAAATGGT	TGCCATCTCA	GGAGTAGATG	GCCCCGGCTCA	CTTCTGGTTA	TCTGTCACCC	2640
TGAGCCCCATG	AGCTGCCTT	TAGGGTACAG	ATTGCCTACT	TGAGGACCTT	GGCCGCTCTG	2700
TAAGCATCTG	ACTCATCTCA	GAAATGTCAA	TTCTTAAACA	CTGTGGCAAC	AGGACCTAGA	2760
ATGGCTGACG	CATTAAGGTT	TTCTTCTTGT	GTCCTGTTCT	ATTATTGTTT	TAAGACCTCA	2820

GTAACCATTT	CAGCCTCTTT	CCAGCAAACC	CTTCTCCATA	GTATTTCACT	CATGGAAGGA	2880
TCATTTATGC	AGGTAGTCAT	TCCAGGAGTT	TTGGTCTTT	TCTGTCTCAA	GGCATTGTGT	2940
GTTTGTTC	GGGACTGGTT	TGGGTGGGAC	AAAGTTAGAA	TTGCCTGAAG	ATCACACATT	3000
CAGACTGTTG	TGTCTGTGGA	TTTTAGGAG	TGGGGGGTGA	CCTTCTGGT	CTTGCACCTT	3060
CCATCCTCTC	CCACTTCCAT	CTGGCATCCC	CACGCGTTGT	CCCCTGCACT	TCTGGAAGGC	3120
ACAGGGTGCT	GCTGCTTCCT	GGTCTTGCC	TTTGCTGGC	CTTCTGTGCA	GGACGCTCAG	3180
CCTCAGGGCT	CAGAAGGTGC	CAGTCCGGTC	CCAGGTCCCT	TGTCCTTCC	ACAGAGGCCT	3240
TCCTAGAAGA	TGCATCTAGA	GTGTCAGCCT	TATCAGTGT	TAAGATTTT	CTTTTATTTT	3300
TAATTTTTT	GAGACAGAAT	CTCACTCTCT	CGCCCAGGCT	GGAGTGCAAC	GGTACGATCT	3360
TGGCTCAGTG	CAACCTCCGC	CTCCTGGGTT	CAAGCGAATC	TCGTGCCTCA	GCCTCCGGAG	3420
TAGCTGGGAT	TGCAGGCACC	CGCCACCACG	CCTGGCTAAT	TTTTGTATTT	TTAGTAGAGA	3480
CGGGGTTCA	CCATGTTGGT	CAGGCTGGTC	TCGAACCTCCT	GACCTCAGGT	GATCCACNTT	3540
GGCCTCCGAA	AGTGCTGGGA	TATACAAGGC	GTGAGCCACC	AGCCAGGCCA	AGATAATTNTT	3600
NTAAAGNNAG	CITCCGGANG	ACATGAAATA	ANGGGGGTT	TTGTTGTITA	GTAACATTING	3660
GCTTGTATAT	ATCCCCAGGC	CAAATNGCAN	GNGACACAGG	ACAGCCATAG	TATAGTGTGT	3720
CACTCGTGGT	TGGTGTCCCT	TCATGGTTCT	GCCCTGTCAA	AGGTCCCTAT	TTGAAATGTG	3780
TTATAATACA	AACAAGGAAG	CACATTGTGT	ACAAAATACT	TATGTATTTA	TGAATCCATG	3840
ACCAAATTAA	ATATGAAACC	TTATATAAAA	AAAAAAAAAA	A		3881

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	Lys
1															15

Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro	Gly	Pro
20															30

Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 35 40 45
 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 50 55 60
 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 65 70 75 80
 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 85 90 95
 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr Gln Trp Asn Asp Leu Leu Phe
 100 105 110
 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 115 120 125
 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 130 135 140
 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 145 150 155 160
 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 165 170 175
 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 180 185 190
 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 195 200 205
 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
 210 215 220
 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 225 230 235 240
 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 245 250 255
 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 260 265 270
 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 275 280 285
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 290 295 300
 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 305 310 315 320
 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 325 330 335
 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 340 345 350
 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 355 360 365
 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 370 375 380
 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
 385 390 395 400
 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser End
 405 410 411

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGACCTCCT	TTTCTGCTTG	CGCTGCACCA	GGTGTGATTG	AGGTGAAGTG	GAGCTAAGTC	60
CCTGCACCAC	GACCAGAAAC	ACAGTGTGTC	AGTGCAGAAGA	AGGCACCTTC	CGGGAAAGAAG	120
ATTCTCCTGA	GATGTGCCGG	AAAGTGCAGCA	CAGGGTGTCC	CAGAGGGATG	GTCAAGGTG	180
GTGATTGTAC	ACCCCTGGAGT	GACATCGAAT	GTGTCCACAA	AGAATCAGGC	ATCATCATAG	240
GAGTCACAGT	TGCAGCCGTA	GTCTTGATTG	TGGCTGTGTT	TGTTTGCAAG	TCTTTACTGT	300
GGAAGAAAGT	CCTTCCTTAC	CTGAAAGGCA	TCTGCTCAGG	TGGTGGTGGG	GACCCTGAGC	360
GTGTGGACAG	AAGCTCACAA	CGACCTGGGG	CTGAGGACAA	TGTCCCTCAAT	GAGATCGTGA	420
GTATCTTGCA	GCCCACCCAG	GTCCTGAGC	AGGAAATGGA	AGTCCAGGAG	CCAGCAGAGC	480
CAACAGGTGT	CAACATGTTG	TCCCCCGGGG	AGTCAGAGCA	TCTGCTGGAA	CCGGCAGAAG	540
CTGAAAGGTC	TCAGAGGAGG	AGGCTGCTGG	TTCCAGCAAA	TGAAGGTGAT	CCCACTGAGA	600
CTCTGAGACA	GTGCTTCGAT	GACTTTGCAG	ACTTGGTGCC	CTTTGACTCC	TGGGAGCCGC	660
TCATGAGGAA	GTTGGGCCTC	ATGGACAATG	AGATAAAAGGT	GGCTAAAGCT	GAGGCAGCGG	720
GCCACAGGGA	CACCTTGTAC	ACGATGCTGA	TAAAGTGGGT	CAACAAAACC	GGGCGAGATG	780
CCTCTGTCCA	CACCTGCTG	GATGCCCTGG	AGACGCTGGG	AGAGAGACTT	GCCAAGCAGA	840
AGATTGAGGA	CCACTTGTG	AGCTCTGGAA	AGTCATGTA	TCTAGAAGGT	AATGCAGACT	900
CTGCCATGTC	CTAAGTGTGA	TTCTCTTCAG	GAAGTCAGAC	CTTCCCTGGT	TTACCTTTTT	960
TCTGGAAAAAA	GCCCAACTGG	ACTCCAGTCA	GTAGGAAAGT	GCCACAATTG	TCACATGACC	1020
GGTACTGGAA	GAAACTCTCC	CATCCAACAT	CACCCAGTGG	AT		1062

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val
1					5				10					15	
Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu
					20				25					30	
Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys

35	40	45
Arg Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro		
50	55	60
Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly		
65	70	75
Val Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys		
85	90	95
Ser Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser		
100	105	110
Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro		
115	120	125
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro		
130	135	140
Thr Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro		
145	150	155
Thr Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu		
165	170	175
Pro Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala		
180	185	190
Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe		
195	200	205
Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu		
210	215	220
Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly		
225	230	235
His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr		
245	250	255
Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu		
260	265	270
Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser		
275	280	285
Gly Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser		
290	295	300